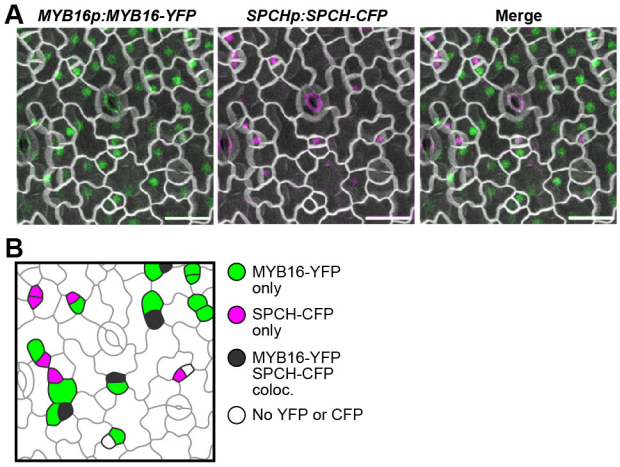
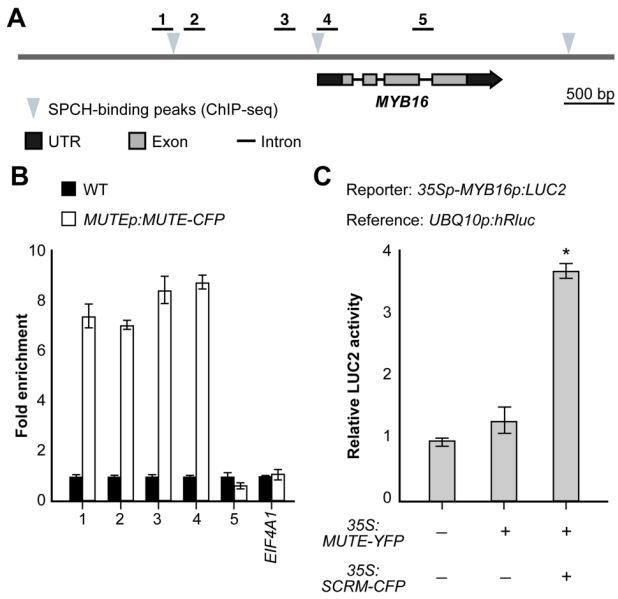


Supplemental Figure S1. MYB16 is preferentially localized to stomatal lineage ground cells (SLGCs). (Supports Figure 1)

(A) An example of images used for quantifying localization preference in **Figure 1B**. MYB16-YFP (green) and SPCH-CFP (magenta) in a wild-type (WT) 7 days post-germination (dpg) true leaf. Cell outline marked by RC12A-mCherry (gray). Scale bars, 20 μm.

(B) A diagram showing meristemoid–SLGC pairs in **(A)**. The colors represent the fluorescent signals in the cells. Green, MYB16-YFP; magenta, SPCH-CFP; black, both MYB16 and SPCH; white, no signal detected.

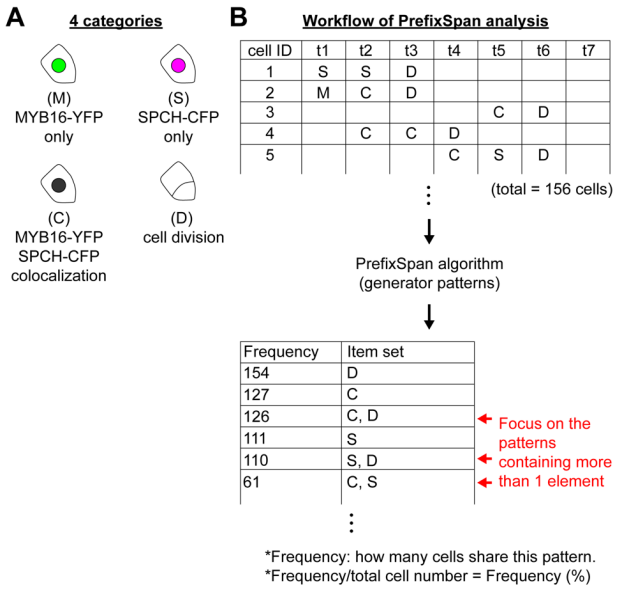


Supplemental Figure S2. MUTE binds to the *MYB16* promoter and upregulates its expression *in vitro*. (Supports Figure 1)

(A) Diagram of *MYB16* genome region. Arrow heads indicate SPCH-binding peaks obtained from SPCH ChIP-seq data (Lau et al., 2014) as shown in **Figure 1D**. The five amplicons (black bars) were designed for the ChIP-qPCR assay in **(B)**.

(B) MUTE binds to the defined *MYB16* promoter region as does SPCH. 4-dpg *MUTEp:MUTE-CFP* seedlings were used to perform ChIP-qPCR by GFP-trap beads. Two biological replicates showed similar results. *EIF4A1* is a negative control. Data are means (SD).

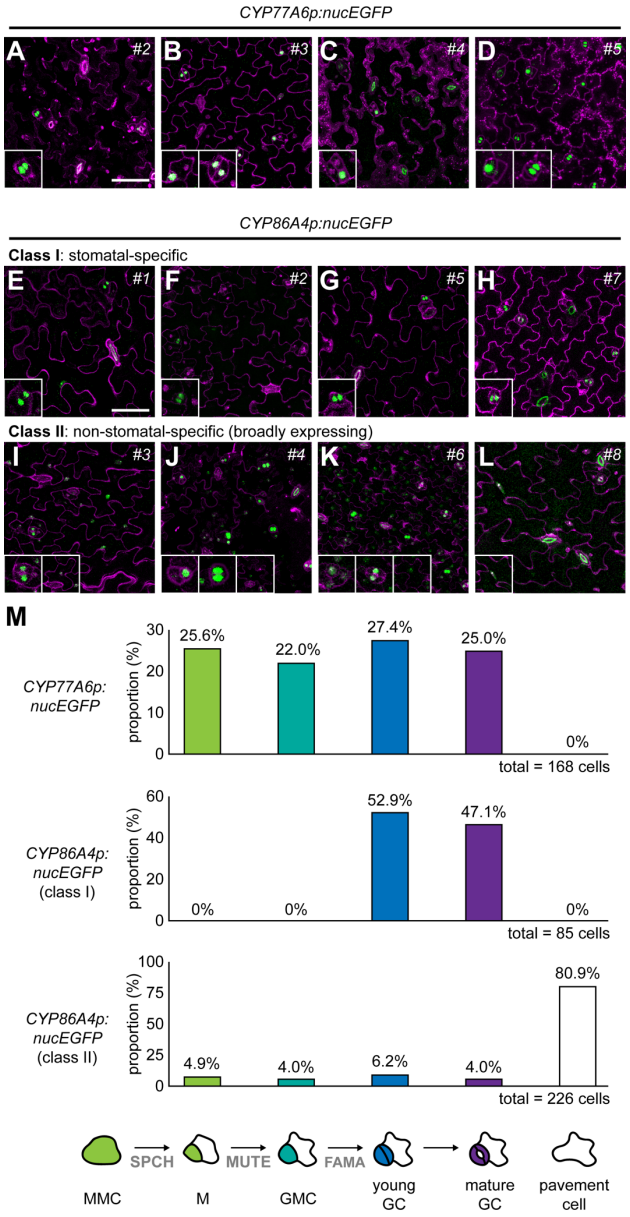
(C) MUTE upregulates *MYB16* expression with SCRM/ICE1. The same MYB16 reporter and SCRM/ICE1 expression clone were used as shown in **Figure 1F** and **1G**. The luciferase assay was performed in 3-week-old WT protoplasts. Four biological replicates showed similar results. *, $p < 0.001$, by Student's t-test. Data are means (SD).



Supplemental Figure S3. The workflow of the analysis of MYB16 and SPCH dynamics using PrefixSpan. (Supports Figure 4)

(A) Cell states in confocal time-lapse images were defined as 4 categories based on the fluorescence signal and cell plate formation.

(B) Behaviors of the cells were analyzed by the PrefixSpan algorithm. First, the 156 cells with different states were recorded across 7 time points (the time intervals between points are 8 or 16 h). Second, the matrix was applied to the PrefixSpan algorithm with generator patterns (Python). Finally, patterns containing > 1 element in the output matrix were produced. A total of 57 patterns were generated with frequency (number of cells with the designed pattern). The percentage frequency (%) in **Figure 4** was calculated as frequency divided by total cell number (156 cells).



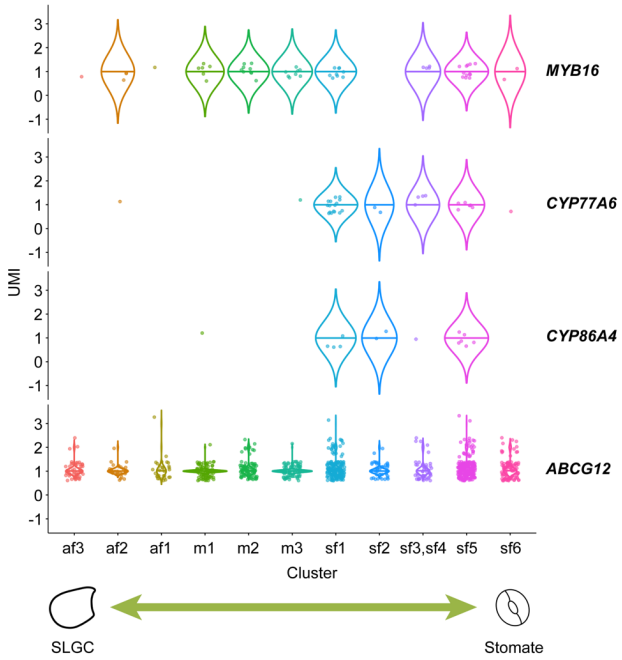
Supplemental Figure S4. Quantification of the *CYP77A6* and *CYP86A4* transcription patterns.
(Supports Figure 4)

(A) to **(D)** Confocal images of 4 independent T1 lines with *CYP77A6* promoter-driven nuclear enhanced GFP (*CYP77A6p:nucEGFP*). All independent lines show similar results that *CYP77A6* expression is stomatal lineage-specific. The GFP signals were found in meristemoids, guard mother cells and guard cells. 4 of 7 individual lines are shown here.

(E) to **(L)** Confocal images of several independent T1 lines of *CYP86A4p:nucEGFP*. Class I **(E)** to **(H)** shows *CYP86A4* expression is guard cell-specific. Class II **(I)** to **(L)** shows *CYP86A4* is broadly expressed in all epidermal cells. 8 of 8 individual lines are shown here.

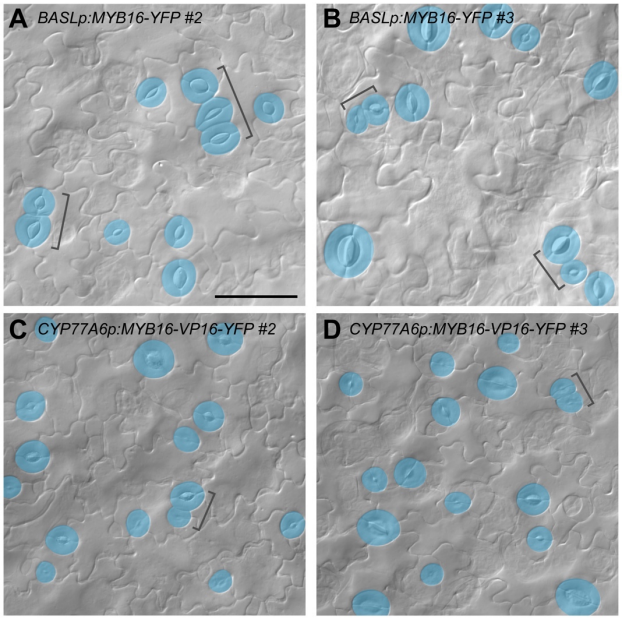
(M) Quantification of nuclear EGFP signal indicates that *CYP77A6* is specifically expressed in stomatal lineage cells, while *CYP86A4* is either specifically expressed in guard cells (class I) or broadly expressed in epidermal cells (class II). MMC, meristemoid mother cell; M, meristemoid; GMC, guard mother cell; GC, guard cell.

For **(A)** to **(L)**, shared scale bars, 50 μm, in **(A)** and **(E)**. Whole-leaf confocal images of 4-dpg cotyledons and 8-dpg true leaves were used in **(M)**. The quantification was calculated from cells with type-specific signals divided by fluorescence positive cells. Total of 168 cells in **(A)** to **(D)**, 85 cells in **(E)** to **(H)**, and 226 cells in **(I)** to **(L)**.



Supplemental Figure S5. Expression patterns of the MYB16-targeted genes from a single-cell perspective (Lopez-Anido et al., 2021). (Supports Figure 4)

Violin plots show a range of gene expression profiles of *MYB16* and its downstream targets, *CYP77A6*, *CYP86A4* and *ABCG12*. *CYP77A6* and *CYP86A4* transcript levels are higher in cells with stomatal fate. sf, stomatal fate; m, meristemoid; af, alternative fate.

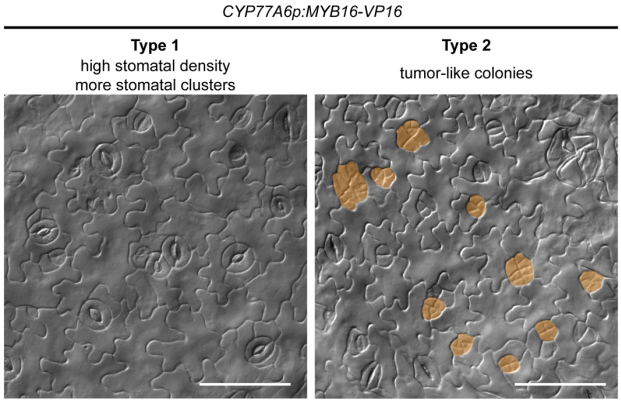


Supplemental Figure S6. The ectopic expression of *MYB16* results in the formation of stomatal clusters. (Supports Figure 4)

(A) and **(B)** DIC images of lower epidermis of 10-dpg *BASLp:MYB16-YFP* cotyledons.

(C) and **(D)** DIC images of lower epidermis of 10-dpg *CYP77A6p:MYB16-VP16-YFP* true leaves.

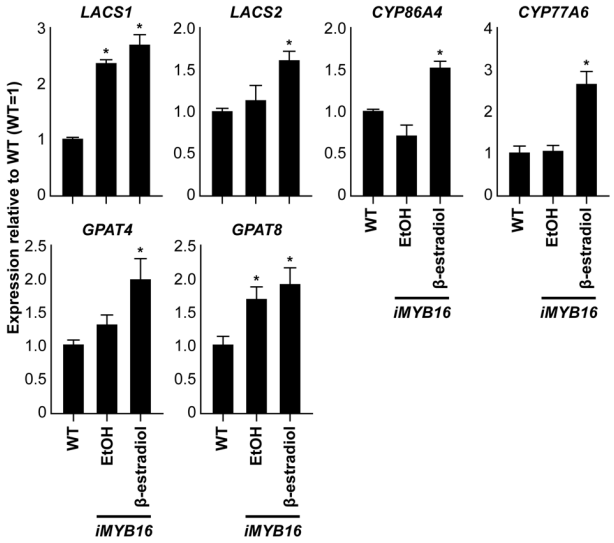
Different from lines shown in **Figure 4H** and **4I**, 2 of 3 independent lines of each background are shown here. Stomatal clusters are indicated by brackets, and mature guard cells are pseudo-colored in blue. For **(A)** to **(D)**, shared scale bar, 50 μm, in **(A)**.



Supplemental Figure S7. Two types of stomatal phenotypes in *CYP77A6p:MYB16-VP16*.

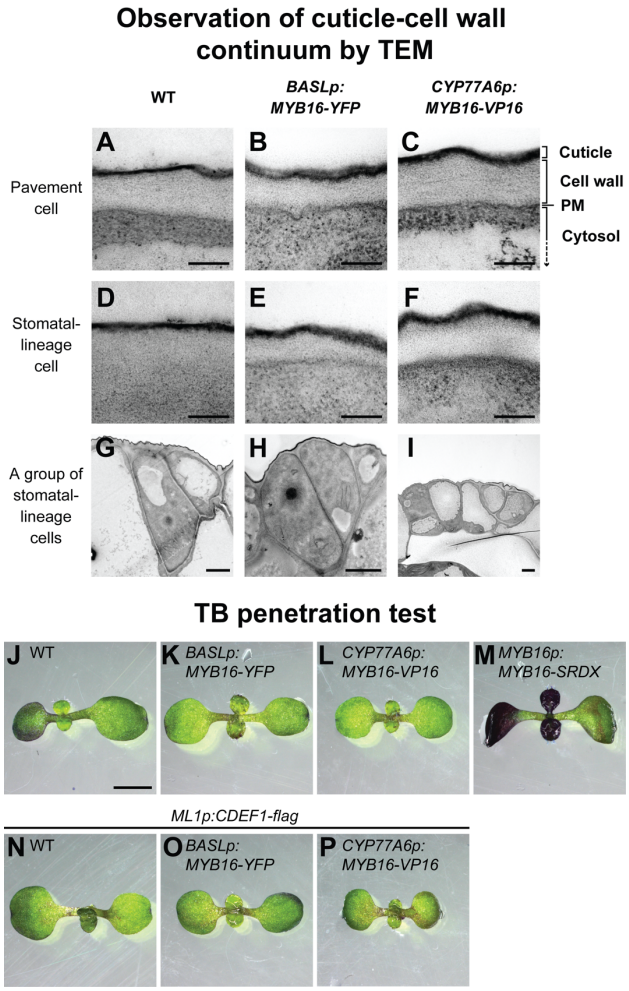
(Supports Figure 4)

DIC images of 10-dpg true leaves of *CYP77A6p:MYB16-VP16*. Type 1 shows higher density of mature guard cells and more frequent cluster events. Type 2 shows tumor-like colonies (small cell clusters, pseudo-colored in orange) and lower density of mature guard cells, which explains the wide range of stomatal density and index seen in **Figure 4M and 4N**. Scale bars, 50 μm.



Supplemental Figure S8. Cutin-related genes are upregulated after induction in the *iMYB16* lines. (Supports Figure 5)

Relative mRNA expression of cuticle biosynthesis genes in the *iMYB16* lines (*iMYB16 #3*) with 10-dpg WT as a standard (WT equal to 1). All selected genes for cutin biosynthesis were upregulated after 4 days of 50 μM β-estradiol treatment. *, $p < 0.01$, by Student t-test. Data are means (SD).



Supplemental Figure S9. Phenotypes of ectopic *MYB16* lines revealed by TEM and a TB penetration assay. (Supports Figure 5)

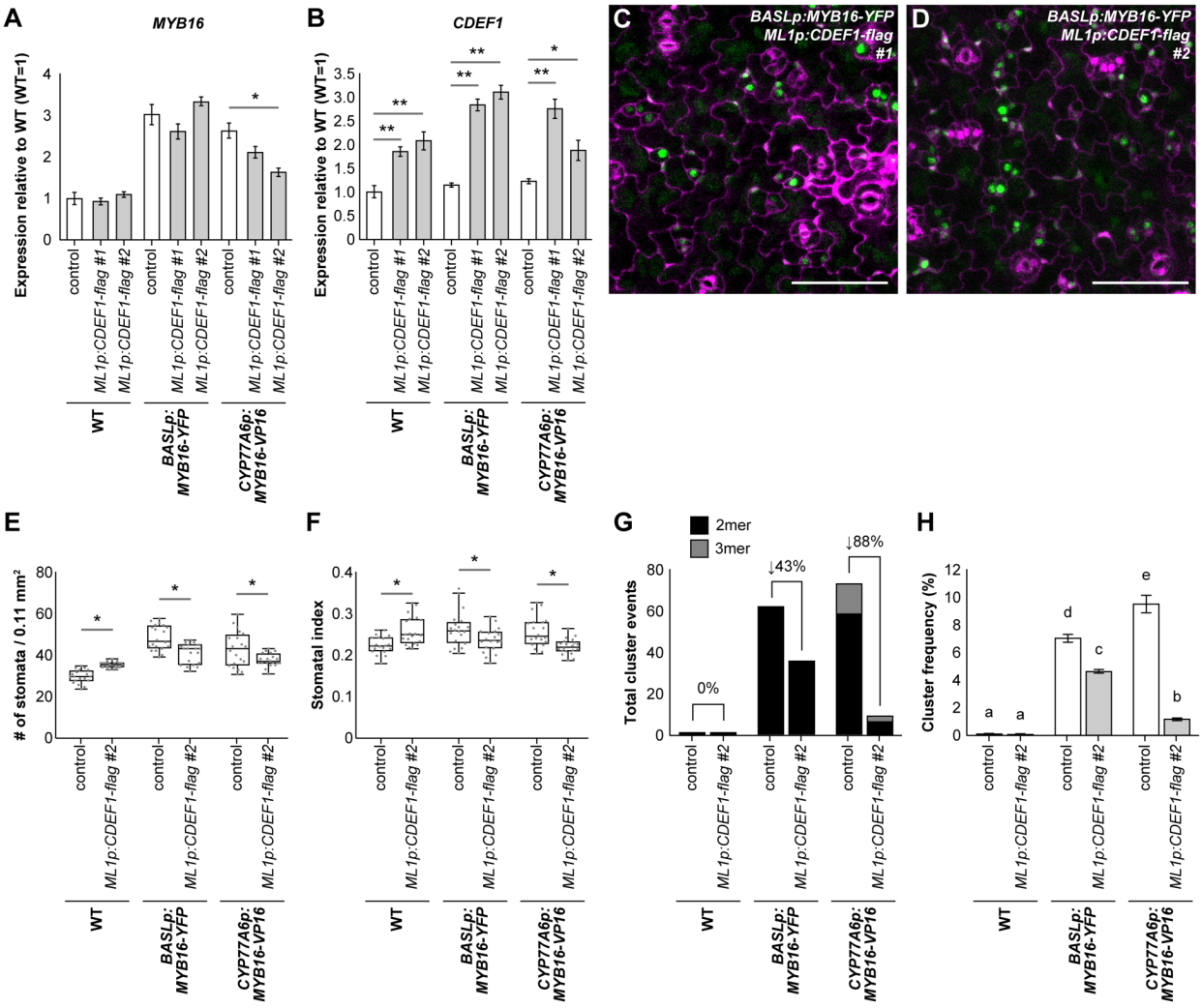
(A) to **(F)** Images by transmission electron microscopy (TEM) of 7-dpg true leaves of WT **(A)** and **(D)**, *BASLp:MYB16-YFP* **(B)** and **(E)**, and *CYP77A6p:MYB16-VP16* **(C)** and **(F)**. The cuticle (electron-dense region at the top) of pavement cells or stomatal-lineage cells is thicker in *BASLp*- and *CYP77A6p*-driven *MYB16* lines than in WT plants.

(G) to **(I)** TEM images focusing on groups of stomatal-lineage cells of 7-dpg true leaves of WT **(G)**, *BASLp:MYB16-YFP* **(H)** and *CYP77A6p:MYB16-VP16* **(I)**. Abnormally small cell cluster (tumor-like) were found in the *MYB16* ectopic lines, especially in *CYP77A6p:MYB16-VP16*.

(J) to **(M)** Toluidine blue (TB) test on 7 dpg seedlings of WT, *BASLp:MYB16-YFP*, *CYP77A6p:MYB16-VP16* and *MYB16p:MYB16-SRDX*.

(N) to **(P)** Toluidine blue (TB) test on 7 dpg seedlings of WT, *BASLp:MYB16-YFP*, *CYP77A6p:MYB16-VP16* after ectopically introducing CDEF1 into epidermis by *ML1* promoter.

For **(A)** to **(F)**, scale bars represent 200 nm. For **(G)** to **(I)**, scale bars represent 2 μm. For **(J)** to **(P)**, the shared scale bar in **(J)** represents 2 mm.



Supplemental Figure S10. Introducing the cutinase gene *CDEF1* into the leaf epidermis rescues the stomatal phenotype in the ectopic *MYB16* lines. (Supports Figure 5)

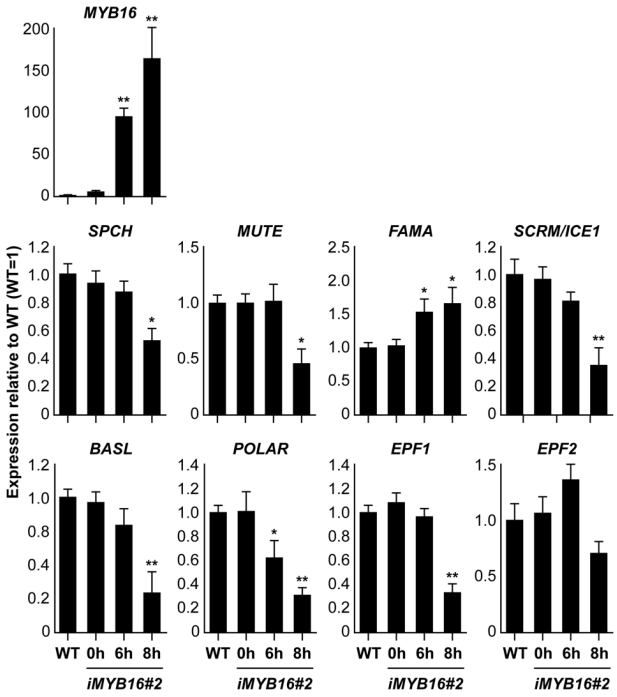
(A) and **(B)** Relative mRNA expression of *MYB16* **(A)** and *CDEF1* **(B)**. 7-dpg WT is used as a reference (equal to 1). Both *MYB16* and *CDEF1* were not silent in the double transgenic lines but *MYB16* expression was reduced in *CYP77A6p:MYB16-VP16/ML1p:CDEF1-flag* #2. *, $p < 0.05$; **, $p < 0.01$, by Student's t-test. Data are means (SD).

(C) and **(D)** Confocal images of 8-dpg true leaves of *BASLp:MYB16-YFP/ML1p:CDEF1-flag*. Two individual lines show MYB16-YFP expression in stomatal lineage cells. Scale bars, 50 μm.

(E) and **(F)** Quantification of stomatal density **(E)** and stomatal index **(F)** by another CDEF1-transgenic line #2 in each background show the partial rescue. n = 20 10-dpg seedlings. *, $p < 0.05$, by Wilcoxon signed-rank test. Data are medians (interquartile range).

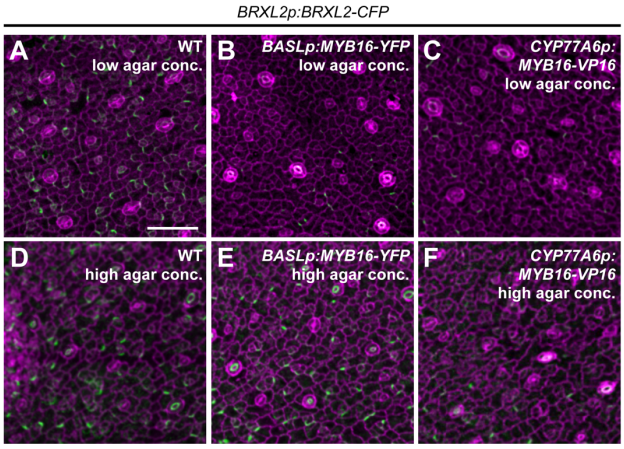
(G) and **(H)** The stomatal clusters **(G)** and cluster frequency **(H)** by CDEF1-transgenic line #2 in each background show cluster reduction. For **(G)**, the value obtained from the sum of the events of 20 lower-epidermis samples. Rescue percentage is the difference of the cluster event between control and *ML1p:CDEF1-flag* divided by the event number in control. For **(H)**, cluster frequency is cluster event number divided by stomatal group number. $p < 0.05$. One-way ANOVA with Tukey post-hoc test. Data are means (SE).

Total 4 individual lines of each background were collected and characterized. Line one (#1) were presented in **Figure 5M** to **5Q**.



Supplemental Figure S11. Expression of genes related to stomatal development in the *iMYB16* lines after a short-term induction of *MYB16* expression, as revealed by qRT-PCR. (Supports Figure 6)

Relative mRNA expression of stomatal development-related genes in 7-dpg WT and *iMYB16* plants after 50 μM β-estradiol induction. 7-dpg WT is used as a reference (equal to 1). *MYB16* expression was highly upregulated after induction. *SPCH* and *MUTE*, transcription factors (TFs) for cell division and commitment, downregulated after 8 h induction. *FAMA*, TF for stomatal maturation, slightly upregulated after 6 h and 8 h induction. *SCRM/ICE1*, a co-TF working with the SPCH, MUTE and FAMA, downregulated after 8 h induction. *BASL* and *POLAR*, proteins participating in the polarity complex during asymmetric division, downregulated after 8 h and 6 h induction, respectively. EPF peptides trigger inhibitory signaling to prevent stomatal formation in SLGCs. *EPF1* significantly and *EPF2* moderately reduced after 8 h induction. Data are means (SD). *, p <0.05. **, p <0.01.



Supplemental Figure S12. Polarity in the ectopic *MYB16* lines is rescued by growth on high-percentage agar growth medium. (Supports Figure 6 and 7)

(A) to **(C)** Confocal images of the polarity marker BRXL2 in 7-dpg true leaves of WT **(A)**, *BASLp:MYB16-YFP #2* **(B)** and *CYP77A6p:MYB16-VP16 #2* **(C)** under low-percentage (0.8%) agar treatment.

(D) to **(F)** Confocal images of the polarity marker BRXL2 in 7-dpg true leaves of WT **(A)**, *BASLp:MYB16-YFP #2* **(B)** and *CYP77A6p:MYB16-VP16 #2* **(C)** under high-percentage (2.4%) agar treatment.

Different from lines shown in **Figure 6** and **7**, 1 of 4 independent lines of each background is shown here. Cell outline is labelled by propidium iodide. Shared scale bar, 50 μm, in **(A)**.

Supplemental Table S1. Primers for DNA manipulation.

DNA constructs for luciferase assay

Backbone	Insert	Primer name	Sequence	Enzyme
pJD301	*MYB16p*	MYB16p-LUCGib-F2	TTGGAGAGAACACGGGGGACAATTTGAGACACATA AACATCTAAG	NEBuilder HiFi
		MYB16p-LUCGib-R	ATGTTTTTGGCATCTTCCATTGTTTTGAGAGCAAAG AAATAAGAACC	NEBuilder HiFi
pENTR/D-TOPO	*SPCH*	SPCH-F_caccNotI	CACCGCGGCCGCATGCAGGAGATAATACCGGATTT TCTTG	NotI
		SPCH_R_AscI	CGGGGCGCGCCCGCAGAATGTTTGCTGAATTTGTT GAGCC	AscI
pENTR/D-TOPO	*SCRM/ICE1*	SCRM-DTOPO-NotI-F	CACCGCGGCCGCCATGGGTCTTGACGGAAACAATG GTG	NotI
		SCRM-CDSns-AscI-R	GTCGGCGCGCCCGATCATACCAGCATACCCTGCTG TATCG	AscI

Note. Underlines in Sequence Column show the recombination or restriction enzyme targeting sites.

DNA constructs for transgenic plants

Backbone	Insert	Primer name	Sequence (Underlines show the enzyme-targeted sites)	Enzyme	Reference
pENTR 5'S		EcoRIcut-NotI_AscI_F	/5Phos/AATTCGCGGCCGCGGCGCGCCG	NotI-AscI	
		EcoRIcut_NotI_AscI_R	/5Phos/AATTCGGCGCGCCGCGGCCGCG	AscI-NotI	

pENTR/D-TOPO	*MYB16*	MYB16F_AT5G15310	CACCATGGGTAGATCACCGTGTTGTGAC		
		MYB16R_AT5G15310	GAACATCGGTGAATCCGACGG		
	3×FLAG	3FLAG-AscI-F	GTGGGCGCGCCGGCATGGATGAACTATACAAAGGTACC	AscI	
		3FLAG-AscI-R	GTCGGCGCGCCAACCAGGCCCCCCCTCG	AscI	
pENTR/D-TOPO	*CYP77A6p: MYB16-VP16*	CYP77A6p-NotI-F	CACCGCGGCCGCTTATCTTCCCGGAATTAGTGAAGACCC	NotI	
		VP16-AscI-R	GTCGGCGCGCCCCCCACCGTACTCGTCAATTCCAAGGGCAT	AscI	
pENTR/D-TOPO	*CYP77A6p*	CYP77A6p-NotI-F	CACCGCGGCCGCTTATCTTCCCGGAATTAGTGAAGACCC	NotI	Oshima et al. (2013)
		CYP77A6p-AscI-R	GTCGGCGCGCCCTTTTAGCTTCTTGTTTTTCTTCTTCTTTTC	AscI	
pENTR/D-TOPO	*CYP86A4p*	CYP86A4p-NotI-F	CACCGCGGCCGCCTTGTGTGTGGTCCGAAGAAGATGAGA	NotI	Oshima et al. (2013)
		CYP86A4p-AscI-NotI-R	CACCGCGGCCGCGGCGCGCCCGTAGCTCTTTTATTATTGTTTCCCAGAG	AscI-NotI	
pENTR/D-TOPO	*CDEF1*	CDEF-NotI-F	CACCGCGGCCGCATGGTCGAGGGAGAGTCCAA	NotI	Takahashi et al. (2010)
		CDEF-AscI-R	GTCGGCGCGCCCATTCACTAACTGGGATATGTTGAACGG	AscI	

pENTR P4-P1R	*BRXL2p*	At3g14000/BRXL2 proF	GGGGACAACTTTGTATAGAAAAGTTGCGAAACAGATC GTTGTGTAGAGTACC	BP clonase
		At3g14000/BRXL2 proR	GGGGACTGCTTTTTTGTACAAACTTGCTCTATCACTC ACTAAAGAGTTTCAATTTCG	BP clonase

Note. Underlines in Sequence Column show the recombination or restriction enzyme targeting sites.

Supplemental Table S2. Details of DNA manipulation.

DNA constructs for reporters

Construct	Entry vectors (inserts)	Destination vectors	Reference
iMYB16	pENTR/D-TOPO (MYB16-3×flag) [2]	pCAMBIA1390(GW) [2]	modified from Kubo et al., (2013)
CYP86A4p:nucEGFP	pENTR/D-TOPO (CYP86A4p)	pBGGN	Kubo et al. (2005)
CYP77A6p:nucEGFP	pENTR/D-TOPO (CYP77A6p)	pBGGN	Kubo et al. (2005)
MYB16p:MYB16-YFP	pDONR P4-P1R (MYB16p)	R4pGWB540	Oshima et al. (2013)
	pENTR/D-TOPO (MYB16)		Nakagawa et al. (2008)
BASLp:MYB16-YFP	pENTR 5'-TOPO (BASLp)	R4pGWB540	Dong et al. (2009)
	pENTR/D-TOPO (MYB16)		Nakagawa et al. (2008)
CYP77A6p:MYB16-VP16-YFP	pENTR/D-TOPO (CYP77A6p:MYB16-VP16)	pHGY	Oshima and Mitsuda (2016)
			Kubo et al. (2005)
AtML1p:CDEF1-flag	pDONR P4-P1R (AtML1p)	R4pGWB610	Davies and Bergmann (2014)
	pENTR/D-TOPO (CDEF1)		Nakagawa et al. (2008)
BRXL2p:BRXL2-CFP	pENTR P4-P1R (BRXL2p)	R4pGWB443	Rowe et al. (2019)
	pENTR/D-TOPO (BRXL2)		Nakagawa et al. (2008)
35S:SPCH-YFP	pENTR/D-TOPO (SPCH)	pH35GY	Lampard et al. (2008)
			Kubo et al. (2005)
35S:SCRM/ICE1-CFP	pENTR/D-TOPO (SCRM/ICE1)	pH35GC	Kubo et al. (2005)

DNA constructs for luciferase assay and CRISPR-Cas9 editting

Construct	Description	Reference
Mini35S-MYB16p:LUC2	~3 kb MYB16 promoter was inserted into pJD301 containing *mini35S:LUC2* and *UBQ10p:hREN* by KpnI (NEB) and HiFi DNA Assembly Master Mix (NEB).	Luehrsen et al. (1992)
Myb16-crispr	For generation of *myb16-crispr* lines, the guide RNA (gRNA), `GACAAATTGGGTTTGAAGAA` was introduced into plasmid containing AtU6-26-sgRNA by BsaI (NEB). The fragment was then introduced into pCAMBIA1300-221 containing *YAOp:Cas9* by SpeI and NheI.	Yan et al. (2015)

Note. 1) Constructs were created by Gateway (Invitrogen) cloning with pENTR 5'-TOPO, pENTR/D-TOPO and pDONR P4-P1R plasmids as backbones. To facilitate cloning processes, we modified pENTR 5'-TOPO by EcoRI (NEB) to introduce NotI and AscI sites; the resulting plasmid was called pENTR 5'S. Genes were cloned into pENTR/D-TOPO plamids by using conventional TOPO isomerase (Invitrogen) or by restriction enzyme digestion with NotI and AscI (NEB) depending on the primer design listed in Supplemental Table S1.

2) pCAMBIA1390(GW) containing 35S:XVE-LexA, a gift from Dr. Shih-Long Tu's lab (IPMB, Academia Sinica). 3×flag fragment was obtained using modified pCAMBIA1390(HA-GFP-FLAG) (Wu et al., 2016) as a backbone.

Supplemental Table S3. Details of plant materials.

Mutant or transgenic line	Description
myb16-crispr	Generated by introducing pCAMBIA1300-221 containing *YAOp:Cas9* and the small guide RNA (sgRNA) driven by the *AtU6* promoter (Yan et al., 2015). After selection to Cas9-free T4 plants, the plants were used for phenotyping.
amiR-MYB16/ myb106-2	Oshima et al., 2013. 2 independent lines were characterized.
MYB16p:MYB16-YFP; SPCHp:SPCH-CFP; ML1p:RC12A-mCherry	Transgenic line expressing three markers. Generated by crossing *MYB16p:MYB16-YFP* (Ho et al., 2021) and *SPCHp:SPCH-CFP*; *ML1p:RC12A-mCherry* (Davies and Bergmann, 2014).
SPCHp:SPCH-CFP	Davies and Bergmann, 2014.
MUTEp:MUTE-CFP	Davies and Bergmann, 2014.
iMYB16	Transgenic line containing *35S:XVE* and *LexAp:MYB16-3xflag* to overexpress *MYB16* under β-estradiol treatment. 4 independent lines (T3) were isolated and characterized.
CYP77A6p:nucEGFP	Transgenic line expressing nucEGFP under the control of the *CYP77A6* promoter. 7 independent lines (T1) were isolated and characterized.
CYP86A4p:nucEGFP	Transgenic line expressing nucEGFP under the control of the *CYP86A4* promoter. 8 independent lines (T1) were isolated and characterized.

BASLp:MYB16-YFP	Transgenic line expressing MYB16 under *BASL* promoter to ectopically introduce MYB16 during asymmetric division. 3 independent lines (T1 to T4) were isolated and characterized.
CYP77A6p:MYB16-VP16	Oshima and Mitsuda, 2016.
CYP77A6p:MYB16-VP16-YFP	Transgenic line derived from *CYP77A6p:MYB16-VP16* (Oshima and Mitsuda, 2016) by adding a fluorescent tag at C-terminal region of VP16. 2 independent lines (T3 and T4) were isolated and characterized.
BASLp:MYB16-YFP; ML1p:RC12A-mCherry	Transgenic line expressing two markers. Generated by crossing *BASLp:MYB16-YFP* and *ML1p:RC12A-mCherry* (Davies and Bergmann, 2014).
BRXL2p:BRXL2-CFP	Transgenic line expressing *BRXL2* polarity marker under native promoter. 4 independent lines (T2) were isolated and characterized.
BRXL2p:BRXL2-CFP; BASLp:MYB16-YFP	Transgenic line expressing *BRXL2* polarity marker under native promoter. Generated by transforming *BRXL2p:BRXL2-CFP* into *BASLp:MYB16-YFP* background. 4 independent lines (T2) were isolated and characterized.
BRXL2p:BRXL2-CFP; CYP77A6p:MYB16-VP16	Transgenic line expressing *BRXL2* polarity marker under native promoter. Generated by transforming *BRXL2p:BRXL2-CFP* into *CYP77A6p:MYB16-VP16* background. 4 independent lines (T2) were isolated and characterized.
ML1p:CDEF1-flag	Transgenic line ectopically expressing *CDEF1* cutinase under epidermal-specific promoter. 5 independent lines (T2) were isolated and 4 of them were characterized.
ML1p:CDEF1-flag; BASLp:MYB16-YFP	Transgenic line ectopically expressing *CDEF1* cutinase under epidermal-specific promoter. Generated by transforming *ML1p:CDEF1-flag* into *BASLp:MYB16-YFP* background. 5 independent lines (T2) were isolated and 4 of them were characterized.

ML1p:CDEF1-flag; CYP77A6p:MYB16-VP16	Transgenic line ectopically expressing *CDEF1* cutinase under epidermal-specific promoter. Generated by transforming *ML1p:CDEF1-flag* into *CYP77A6p:MYB16-VP16* background. 5 independent lines (T2) were isolated and 4 of them were characterized.
35Sp:EPF2	Transgenic line overexpressing *EPF2* under the control of the 35S promoter. 20 independent lines (T1) were isolated and characterized.
35Sp:EPF2; BASLp:MYB16-YFP	Transgenic line overexpressing *EPF2* under 35S promoter. Generated by transforming 35S*p:EPF2* into *BASLp:MYB16-YFP* background. 20 independent lines (T1) were isolated and characterized.

Note. All mutants and transgenic lines were in the Col-0 background.

Supplemental Table S4. Primers used in this study.

qRT PCR: mRNA expression level

Gene	Forward/Reverse	Sequence
MYB16	Forward	TTGGACAACAAAACCACACGAAG
	Reverse	TGTAGATGTCGGAGATTCAAGCT
LACS1	Forward	TGGAGACAAAACCTTTCGACGT
	Reverse	TGAGCGTCGCAGTCACTAAGTC
LACS2	Forward	CTCAAGATGTCCCCTCATTGC
	Reverse	GACTCGAAGCTGTTGCCATAGA
CYP86A4	Forward	CCGCTCTTGAATTCACAACAAG
	Reverse	GTTCTGCATTGTCTTGAGCCGTTGC
CYP77A6	Forward	CGAAGAAATTTAACCCGGATCG
	Reverse	TATGTCCGCTTCCTCCTTACCC
GPAT4	Forward	CGATTTCATGTCCATTTGCAAG
	Reverse	GGCTGATTTGGTCTCATGCACC
GPAT8	Forward	GCCAACATGAGAAAACTTCTCG
	Reverse	CGTCGTGCCTTCCGGACATATC
CDEF1	Forward	AACCGGTCGGTTTAGCAAC
	Reverse	GCTTGTGCCTGTGATGCTC
SPCH	Forward	ATCATAGGAGGAGTTGTGGAG
	Reverse	TAGAACAGGCGGTGAAGGAC
MUTE	Forward	CGATCATCGGAGGAGTGATAGA
	Reverse	AAGGGAAAGATGGTCGGTTTAG
FAMA	Forward	GAACAAACCGTCCTCTACTCC
	Reverse	ATATTTCCCAGGTTAGAGCTTCC
SCRM1/ICE1	Forward	ACACCTACACCGCAAACTC
	Reverse	TCTACGACCACAGAACATATGAATG
BASL	Forward	AGACGGAATCGTCCTCGGAA
	Reverse	CCTTGACATGAAGTGTTATCG
POLAR	Forward	CCTGAATAAGAGTAAAGAGCCGG
	Reverse	GCATTCGCAGGTTTGTCATC

EPF1	Forward	CTTGGCTAGGCATTTACCAACA
	Reverse	CAATGCCCCGGTCATTCCTA
EPF2	Forward	TTTGGTCGTTAACTCCATTCGC
	Reverse	CTTTTCTCCGCCATTGACCGT

ChIP-qRT PCR

Gene (promoter region)	Forward/Reverse	Sequence
MYB16p (region 1)	Forward	AGGCTAACTTGAAGTATGTAAGGACCATAC
	Reverse	AAGAAGAGAGAGGAAGAGAGCTCATGGATC
MYB16p (region 2)	Forward	TGTAAAATCTCTTTAATGTCACCGTTTGCC
	Reverse	ACCTCATCTTGTGATCTTATATGGTTGTGG
MYB16p (region 3)	Forward	GAAGCTAGCTAACAAACCAAAGGCATC
	Reverse	CAGCTTCTAGCACTCTAATATCTTCATCCG
MYB16p (region 4)	Forward	TGAGCCGGGGAAAAAGGGATTC
	Reverse	GGCTACAGTTGTGGAAATGTTACAAGTG
MYB16p (region 5)	Forward	TTGGACAACAAAACCACACGAAG
	Reverse	TGTAGATGTCGGAGATTCAAGCT
EIF4A1	Forward	TGTTTTGCTTCGTTTCAAGGATTCTTC
	Reverse	GCATTTTCCCGATTACAACGAGG

CRISPR: guide RNA (gRNA)

Gene	Forward/Reverse	Sequence
MYB16-gRNA	Forward	ATTGACAAATTGGGTTTGAAGAA
	Reverse	AAACTTCTTCAAACCCAATTTGT

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